

## SEQUENCE LISTING

<110> Ajinomoto Co. Inc.

<120> Method for Producing L-Amino Acid Using Methylophil

<130> OP1629

<150> JP 2002-336346

<151> 2002-11-20

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 1

agggaattcc ccgttctgga taatgttttt tgcgcgcac

39

<210> 2

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 2

cggatgcac tagagttaac ctgcagggtg aaattgttat ccgctcaca ttccacac 58

<210> 3

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 3

tgacctgcag gtttgcacag aggatggccc atgtt

35

<210> 4

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 4

cattctagat ccctaaactt tacagcaaac cggcat

36

<210> 5

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 5

catttcctgc aggcaaagga gatgagcgta atggtgatca tggaaatctt cattacaggt  
ctgc

60  
64

<210> 6

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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<210> 7

<211> 711

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(711)

<400> 7

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Met	Val	Ile	Met	Glu	Ile	Phe	Ile	Thr	Gly	Leu	Leu	Leu	Gly	Ala	Ser	
1			5					10				15				
ctt	tta	ctg	tcc	atc	gga	ccg	cag	aat	gta	ctg	gtg	att	aaa	caa	gga	96
Leu	Leu	Leu	Ser	Ile	Gly	Pro	Gln	Asn	Val	Leu	Val	Ile	Lys	Gln	Gly	
			20					25				30				
att	aag	cgc	gaa	gga	ctc	att	gcg	ggt	ctt	ctc	gtg	tgt	tta	att	tct	144
Ile	Lys	Arg	Glu	Gly	Leu	Ile	Ala	Val	Leu	Leu	Val	Cys	Leu	Ile	Ser	
			35					40				45				
gac	gtc	ttt	ttg	ttc	atc	gcc	ggc	acc	ttg	ggc	ggt	gat	ctt	ttg	tcc	192
Asp	Val	Phe	Leu	Phe	Ile	Ala	Gly	Thr	Leu	Gly	Val	Asp	Leu	Leu	Ser	
			50				55					60				
aat	gcc	gcg	ccg	atc	gtg	ctc	gat	att	atg	cgc	tgg	ggt	ggc	atc	gct	240
Asn	Ala	Ala	Pro	Ile	Val	Leu	Asp	Ile	Met	Arg	Trp	Gly	Gly	Ile	Ala	
			65				70					75			80	
tac	ctg	tta	tgg	ttt	gcc	gtc	atg	gca	gcg	aaa	gac	gcc	atg	aca	aac	288
Tyr	Leu	Leu	Trp	Phe	Ala	Val	Met	Ala	Ala	Lys	Asp	Ala	Met	Thr	Asn	
							85					90			95	
aag	gtg	gaa	gcg	cca	cag	atc	att	gaa	gaa	aca	gaa	cca	acc	gtg	ccc	336

Lys	Val	Glu	Ala	Pro	Gln	Ile	Ile	Glu	Glu	Thr	Glu	Pro	Thr	Val	Pro		
			100					105					110				
gat	gac	acg	cct	ttg	ggc	ggt	tcg	gcg	gtg	gcc	act	gac	acg	cgc	aac	384	
Asp	Asp	Thr	Pro	Leu	Gly	Gly	Ser	Ala	Val	Ala	Thr	Asp	Thr	Arg	Asn		
			115				120					125					
cgg	gtg	cgg	gtg	gag	gtg	agc	gtc	gat	aag	cag	cgg	gtt	tgg	gta	aag	432	
Arg	Val	Arg	Val	Glu	Val	Ser	Val	Asp	Lys	Gln	Arg	Val	Trp	Val	Lys		
			130				135					140					
ccc	atg	ttg	atg	gca	atc	gtg	ctg	acc	tgg	ttg	aac	ccg	aat	gcg	tat	480	
Pro	Met	Leu	Met	Ala	Ile	Val	Leu	Thr	Trp	Leu	Asn	Pro	Asn	Ala	Tyr		
			145			150				155				160			
ttg	gac	gcg	ttt	gtg	ttt	atc	ggc	ggc	gtc	ggc	gcg	caa	tac	ggc	gac	528	
Leu	Asp	Ala	Phe	Val	Phe	Ile	Gly	Gly	Val	Gly	Ala	Gln	Tyr	Gly	Asp		
			165					170				175					
acc	gga	cgg	tgg	att	ttc	gcc	gct	ggc	gcg	ttc	gcg	gca	agc	ctg	atc	576	
Thr	Gly	Arg	Trp	Ile	Phe	Ala	Ala	Gly	Ala	Phe	Ala	Ala	Ser	Leu	Ile		
			180					185				190					
tgg	ttc	ccg	ctg	gtg	ggt	ttc	ggc	gca	gca	gca	ttg	tca	cgc	ccg	ctg	624	
Trp	Phe	Pro	Leu	Val	Gly	Phe	Gly	Ala	Ala	Ala	Leu	Ser	Arg	Pro	Leu		
			195				200					205					
tcc	agc	ccc	aag	gtg	tgg	cgc	tgg	atc	aac	gtc	gtc	gtg	gca	gtt	gtg	672	
Ser	Ser	Pro	Lys	Val	Trp	Arg	Trp	Ile	Asn	Val	Val	Val	Ala	Val	Val		
			210			215				220							
atg	acc	gca	ttg	gcc	atc	aaa	ctg	atg	ttg	atg	ggt	tag				711	
Met	Thr	Ala	Leu	Ala	Ile	Lys	Leu	Met	Leu	Met	Gly						
			225			230				235							

<210> 8

<211> 236

<212> PRT

<213> Brevibacterium lactofermentum

<400> 8

Met	Val	Ile	Met	Glu	Ile	Phe	Ile	Thr	Gly	Leu	Leu	Leu	Gly	Ala	Ser
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	20		25		30
Ile	Lys	Arg	Glu	Gly	Leu
	35		40		45
Asp	Val	Phe	Leu	Phe	Ile
	50		55		60
Asn	Ala	Ala	Pro	Ile	Val
	65		70		75
Tyr	Leu	Leu	Trp	Phe	Ala
			85		90
Lys	Val	Glu	Ala	Pro	Gln
			100		105
Asp	Asp	Thr	Pro	Leu	Gly
			115		120
Arg	Val	Arg	Val	Glu	Val
			130		135
Pro	Met	Leu	Met	Ala	Ile
			145		150
Leu	Asp	Ala	Phe	Val	Phe
			165		170
Thr	Gly	Arg	Trp	Ile	Phe
			180		185
Trp	Phe	Pro	Leu	Val	Gly
			195		200
Ser	Ser	Pro	Lys	Val	Trp
			210		215
Met	Thr	Ala	Leu	Ala	Ile
			225		230

<210> 9

<211> 712

<212> DNA

<213> Brevibacterium lactofermentum

<220>

<221> CDS

<222> (1)..(375)

<400> 9

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    1             5             10             15
ctt ttg ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga 96
Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly
            20             25             30
att aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct 144
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser
            35             40             45
gac gtc ttt ttg ttc atc gcc gcc acc ttg gcc gtt gat ctt ttg tcc 192
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser
            50             55             60
aat gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt gcc atc gct 240
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala
            65             70             75             80
tac ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac 288
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn
            85             90             95
aag gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc 336
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro
            100            105            110
gat gac acg cct ttg gcc gtg ttc gcc ggt gcc cac tga cacgcgcaac 385
Asp Asp Thr Pro Leu Gly Val Phe Gly Gly Gly His
            115            120            125
cggggtgcggg tggaggtgag cgtcgataag cagcggggttt ggggtgaagcc catgttgatg 445
gcaatcgtgc tgacctggtt gaaccogaat gcgtatttgg acgcgtttgt gtttatcggc 505
ggcgtcggcg cgcaatacgg cgacaccgga cggtaggattt tcgcoctgg cgcgttcgcg 565
gcaagcctga tctggttccc gctggtgggt ttcggcgcag cagcattgtc acgcccgtcg 625
tccagcccca aggtgtggcg ctggatcaac gtcgtcgtgg cagttgtgat gaccgcattg 685
gccatcaaac tgatgttgat ggggttag 712
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<210> 10

<211> 124

<212> PRT

<213> Brevibacterium lactofermentum

<400> 10

Met Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser  
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Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly  
20 25 30  
Ile Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser  
35 40 45  
Asp Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser  
50 55 60  
Asn Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala  
65 70 75 80  
Tyr Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn  
85 90 95  
Lys Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro  
100 105 110  
Asp Asp Thr Pro Leu Gly Val Phe Gly Gly Gly His  
115 120

<210> 11

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 11

cccccgggat ttcttctctc cggtctgctt

30

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 12

taaagcttgg tcagggcggtt ggcggtggcg

30

<210> 13

<211> 1197

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (272)..(1153)

<400> 13

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caattccacg gcgatcggca cccaacgcag tgatcaccag ataatgtgtt gcgatgacag 120  
tgtcaaactg gttattcctt taaggggtga gttgttctta aggaaagcat aaaaaaaca 180  
tgcatacaac aatcagaacg gttctgtctg cttgctttta atgccatacc aaacgtacca 240  
ttgagacact tgtttgcaca gaggatggcc c atg ttc acg gga agt att gtc 292

Met Phe Thr Gly Ser Ile Val

1

5

gcg att gtt act ccg atg gat gaa aaa ggt aat gtc tgt cgg gct agc 340  
Ala Ile Val Thr Pro Met Asp Glu Lys Gly Asn Val Cys Arg Ala Ser

10

15

20

ttg aaa aaa ctg att gat tat cat gtc gcc agc ggt act tcg gcg atc 388  
Leu Lys Lys Leu Ile Asp Tyr His Val Ala Ser Gly Thr Ser Ala Ile

25

30

35

gtt tct gtt ggc acc act ggc gag tcc gct acc tta aat cat gac gaa 436  
Val Ser Val Gly Thr Thr Gly Glu Ser Ala Thr Leu Asn His Asp Glu

40

45

50

55

cat gct gat gtg gtg atg atg acg ctg gat ctg gct gat ggg cgc att 484  
His Ala Asp Val Val Met Met Thr Leu Asp Leu Ala Asp Gly Arg Ile

60

65

70

ccg gta att gcc ggg acc ggc gct aac gct act gcg gaa gcc att agc 532  
Pro Val Ile Ala Gly Thr Gly Ala Asn Ala Thr Ala Glu Ala Ile Ser

75

80

85

ctg acg cag cgc ttc aat gac agt ggt atc gtc ggc tgc ctg acg gta 580



Leu	Thr	Gln	Arg	Phe	Asn	Asp	Ser	Gly	Ile	Val	Gly	Cys	Leu	Thr	Val		
		90					95					100					
acc	cct	tac	tac	aat	cgt	ccg	tcg	caa	gaa	ggg	ttg	tat	cag	cat	ttc	628	
Thr	Pro	Tyr	Tyr	Asn	Arg	Pro	Ser	Gln	Glu	Gly	Leu	Tyr	Gln	His	Phe		
		105					110				115						
aaa	gcc	atc	gct	gag	cat	act	gac	ctg	ccg	caa	att	ctg	tat	aat	gtg	676	
Lys	Ala	Ile	Ala	Glu	His	Thr	Asp	Leu	Pro	Gln	Ile	Leu	Tyr	Asn	Val		
		120			125					130					135		
ccg	tcc	cgt	act	ggc	tgc	gat	ctg	ctc	ccg	gaa	acg	gtg	ggc	cgt	ctg	724	
Pro	Ser	Arg	Thr	Gly	Cys	Asp	Leu	Leu	Pro	Glu	Thr	Val	Gly	Arg	Leu		
				140					145					150			
gcg	aaa	gta	aaa	aat	att	atc	gga	atc	aaa	gag	gca	aca	ggg	aac	tta	772	
Ala	Lys	Val	Lys	Asn	Ile	Ile	Gly	Ile	Lys	Glu	Ala	Thr	Gly	Asn	Leu		
			155					160					165				
acg	cgt	gta	aac	cag	atc	aaa	gag	ctg	gtt	tca	gat	gat	ttt	gtt	ctg	820	
Thr	Arg	Val	Asn	Gln	Ile	Lys	Glu	Leu	Val	Ser	Asp	Asp	Phe	Val	Leu		
		170					175					180					
ctg	agc	ggc	gat	gat	gcg	agc	gcg	ctg	gac	ttc	atg	caa	ttg	ggc	ggg	868	
Leu	Ser	Gly	Asp	Asp	Ala	Ser	Ala	Leu	Asp	Phe	Met	Gln	Leu	Gly	Gly		
		185				190				195							
cat	ggg	gtt	att	tcc	gtt	acg	act	aac	gtc	gca	gcg	cgt	gat	atg	gcc	916	
His	Gly	Val	Ile	Ser	Val	Thr	Thr	Asn	Val	Ala	Ala	Arg	Asp	Met	Ala		
		200			205				210			215					
cag	atg	tgc	aaa	ctg	gca	gca	gaa	gaa	cat	ttt	gcc	gag	gca	cgc	gtt	964	
Gln	Met	Cys	Lys	Leu	Ala	Ala	Glu	Glu	His	Phe	Ala	Glu	Ala	Arg	Val		
				220				225				230					
att	aat	cag	cgt	ctg	atg	cca	tta	cac	aac	aaa	cta	ttt	gtc	gaa	ccc	1012	
Ile	Asn	Gln	Arg	Leu	Met	Pro	Leu	His	Asn	Lys	Leu	Phe	Val	Glu	Pro		
		235					240					245					
aat	cca	atc	ccg	gtg	aaa	tgg	gca	tgt	aag	gaa	ctg	ggg	ctt	gtg	gcg	1060	
Asn	Pro	Ile	Pro	Val	Lys	Trp	Ala	Cys	Lys	Glu	Leu	Gly	Leu	Val	Ala		
		250					255				260						
acc	gat	acg	ctg	cgc	ctg	cca	atg	aca	cca	atc	acc	gac	agt	ggg	cgt	1108	
Thr	Asp	Thr	Leu	Arg	Leu	Pro	Met	Thr	Pro	Ile	Thr	Asp	Ser	Gly	Arg		
		265				270					275						
gag	acg	gtc	aga	gcg	gcg	ctt	aag	cat	gcc	ggg	ttg	ctg	taa			1150	
Glu	Thr	Val	Arg	Ala	Ala	Leu	Lys	His	Ala	Gly	Leu	Leu					

280 285 290  
 agtttaggga gatttgatgg cttactctgt tcaaaagtcg cgcctgg

1197

<210> 14  
 <211> 292  
 <212> PRT  
 <213> Escherichia coli

<400> 14

Met	Phe	Thr	Gly	Ser	Ile	Val	Ala	Ile	Val	Thr	Pro	Met	Asp	Glu	Lys
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Gly	Asn	Val	Cys	Arg	Ala	Ser	Leu	Lys	Lys	Leu	Ile	Asp	Tyr	His	Val
			20					25					30		
Ala	Ser	Gly	Thr	Ser	Ala	Ile	Val	Ser	Val	Gly	Thr	Thr	Gly	Glu	Ser
		35					40					45			
Ala	Thr	Leu	Asn	His	Asp	Glu	His	Ala	Asp	Val	Val	Met	Met	Thr	Leu
	50					55				60					
Asp	Leu	Ala	Asp	Gly	Arg	Ile	Pro	Val	Ile	Ala	Gly	Thr	Gly	Ala	Asn
65					70					75					80
Ala	Thr	Ala	Glu	Ala	Ile	Ser	Leu	Thr	Gln	Arg	Phe	Asn	Asp	Ser	Gly
				85					90					95	
Ile	Val	Gly	Cys	Leu	Thr	Val	Thr	Pro	Tyr	Tyr	Asn	Arg	Pro	Ser	Gln
		100					105					110			
Glu	Gly	Leu	Tyr	Gln	His	Phe	Lys	Ala	Ile	Ala	Glu	His	Thr	Asp	Leu
	115						120				125				
Pro	Gln	Ile	Leu	Tyr	Asn	Val	Pro	Ser	Arg	Thr	Gly	Cys	Asp	Leu	Leu
	130					135					140				
Pro	Glu	Thr	Val	Gly	Arg	Leu	Ala	Lys	Val	Lys	Asn	Ile	Ile	Gly	Ile
145					150					155				160	
Lys	Glu	Ala	Thr	Gly	Asn	Leu	Thr	Arg	Val	Asn	Gln	Ile	Lys	Glu	Leu
			165					170				175			
Val	Ser	Asp	Asp	Phe	Val	Leu	Leu	Ser	Gly	Asp	Asp	Ala	Ser	Ala	Leu
		180						185				190			
Asp	Phe	Met	Gln	Leu	Gly	Gly	His	Gly	Val	Ile	Ser	Val	Thr	Thr	Asn
	195						200				205				
Val	Ala	Ala	Arg	Asp	Met	Ala	Gln	Met	Cys	Lys	Leu	Ala	Ala	Glu	Glu
	210					215					220				

11